Appendix A. Genes identified by microarray analysis to be up-regulated at 4°C in stationary-phase cells

Protein category and gene	Function	Fold Change: *Chan*	*Dovilas*
Cell membrane function			
lmo0195	similar to membrane protein (putative ABC transporter component)	2.2	
lmo0220 (ftsH)	highly similar to cell division protein FtsH	2.65	
lmo0316	similar to hydroxyethylthiazole kinase (ThiM)		2.13
lmo0433 (inlA)	Internalin A		3.15
lmo0495	similar to transmembrane protein		2.13
lmo0540	similar to penicillin-binding protein	3.05	
lmo0581 (met)	putative SAM-dependent methyltransferase	2.17	
lmo0582 (iap)	P60 extracellular protein, invasion associated protein	3.07	
lmo0835	putative peptidoglycan bound protein (LPXTG motif)		2.12
l*mo0872*	similar to antibiotic resistance protein		2.28
lmo0880	similar to wall associated protein precursor (LPXTG motif)		2.16
lmo1250	similar to antibiotic resistance protein	2.08	
lmo1265	weakly similar to oligopeptide ABC transporter AppA (binding protein)		2.66
lmo1637	similar to membrane protein	2.97	
lmo1653	putative cell surface protein		2.23
lmo1682	similar to transmembrane transport proteins		2.02
lmo1713	similar to cell-shape determining proteins	4.98	
l*mo1864*	similar to hemolysin III proteins, putative integral membrane protein	8.26	
lmo2153	similar to flavodoin	4.04	
lmo2396	similar to internalin proteins, putative peptidoglycan bound protein		2.33
lmo2471	similar to NADPH oxidase	2.03	
lmo2505 (spl)	peptidoglycan lytic protein P45	4.36	
lmo2522	similar to hypothetical cell wall binding protein from *B. subtilis*	4.49	
lmo2821	similar to internalin, unknown, putative peptidoglycan bound protein		2.15
lmo2845	similar to transmembrane efflux proteins		2.33

Cell metabolic pathways/Biosynthesis

lmo0012	similar to mevalonate kinases	2.07	
lmo0055 (purA)	highly similar to adenylosuccinate synthetase	3.05	
l*mo0348*	similar to dihydroxyacetone kinase		2.14
l*mo0538*	similar to N-acyl-L-amino acid amidohydrolase	2.07	
lmo0554	similar to NADH-dependent butanol dehydrogenase		2.21
lmo0561	similar to phosphoribosyl-AMP-cyclohydrolase (Hisl2 protein)	2.33	
lmo0562	similar to phosphoribosyl-AMP-cyclohydrolase (Hisl1 protein)	3.11	
lmo0625	putative lipase/acylhydrolase	3.08	
lmo0722	similar to pyruvate oxidase		2.1
l*mo0782*	similar to mannose-specific phosphotransferase (PTS), component IIC		2.39
l*mo0783*	similar to mannose-specific phosphotransferase (PTS), component IIB		2.22
lmo0875	similar to PTS system, beta-glucosidase enzyme IIB component		2.05
lmo0892 (rsbU)	highly similar to serine phosphatase RsbU	5.28	
lmo1003	phosphotransferase system enzyme I	2.43	
lmo1038	weakly similar to molybdenum-guanine dinucleotide	2.46	
lmo1072 (pycA)	highly similar to pyruvate carboxylase	2.65	
lmo1084	similar to DTDP-L-rhamnose synthetase	2.29	
lmo1147	similar to bifunctional cobalamin biosynthesis protein CopB		2.31
lmo1148	highly similar to cobalamin (5'-phosphatase) synthetase		2.41
lmo1149	similar to alpha-ribazole-5'-phosphatase		2.53
lmo1186	similar to ethanolamine utilization protein EutH- *E. coli*		2.02
lmo1187	similar to ethanolamine utilization protein EutQ		2.04
lmo1217	similar to endo-1,4-beta-glucanase and to aminopeptidase	2.03	
lmo1254	similar to alpha, alpha-phosphotrehalase	4.83	
lmo1255	similar to PTS system trehalose specific enzyme IIBC	2.81	
lmo1339	similar to glucose kinase	2.09	
lmo1357	acetyl-CoA carboxylase subunit (biotin carboxylase subunit)	2.1	
lmo1363	similar to geranyltransferase	3.07	
lmo1387	similar to pyrroline-5-carboxylate reductase	2.55	

lmo1391	similar to sugar ABC transporter, permease protein		2.06	
lmo1392	similar to putative proteases		2.66	
lmo1407 (pflC)	pyruvate-formate lyase activating enzyme		2.47	
lmo1476 (hemN)	highly similar to coproporphyrinogne III oxidase		2.19	
l*mo1488*	nicotinate-nucleotide adenylyltransferase		3.29	
lmo1571 (pfk)	highly similar to 6-phosphofructokinase		3.11	
lmo1573 (accD)	highly similar to acetyl-CoA carboxylase beta subunit		4.78	
lmo1579	similar to alanine dehydrogenase			2.1
lmo1600 (aroA)	3-deoxy-D-arabino-heptulosonate 7-phosphate synthetase		4	
lmo1634	similar to alcohol-acetyladehyde dehydrogenase		5.01	
lmo1733	similar to glutamate synthase (small subunit)		5.62	
lmo1734	similar to glutamate synthase (large subunit)		3.63	
l*mo1767 (purM)*	phosphoribosylaminoimidazole synthetase		2.77	
lmo1773 (purB)	adenylsuccinate lyase		2.64	
lmo1775 (pure)	phosphoribosylaminoimidazole carboxylase I		3.08	
lmo1813	similar to phosphoglycerate dehydrogenase		2.13	
lmo1917 (pflA)	similar to pyruvate formate-lyase		4.21	
lmo1926	similar to chorismate mutase		4.87	
lmo1927 (aroB)	similar to 3-dehydroquinate synthase		6.15	
lmo1928 (aroF)	similar to chorismate synthase		5.54	
lmo1925 (hisC)	similar to histidinol-phosphate aminotransferase		3.56	
lmo1924 (tyrA)	similar to prephenate dehydrogenase		3.9	
lmo1923 (aroE)	similar to 5-enolpyruvylshikimate-3-phosphate dehydrogenase		4.51	
lmo1936 (gpsA)	similar to NAD(P)H-dependent glycerol-3-phosphate dehydrogenase		4.17	
lmo1954 (drm)	similar to phosphopentomutase		2.99	
l*mo1953 (pnp)*	similar to purine-nucleoside phosphorylase		2.84	
l*mo1993*	similar to pyrimidine-nucleoside phosphorylase		2.34	
lmo2038 (murE)similar to UDP-N-acetylmuramoylalanyl-D-glutamate-2,6-diaminopimelate ligase		2.09		
l*mo2202*	similar to 3-oxyacyl-carrier proteins synthase		2.16	
lmo2211 (hemH)	similar to ferrochelatase		7.58	

l*mo2337*	similar to regulatory protein DeoR family		2.05
l*mo2390*	similar to hypothetical thioredoxin reductase	3.1	
l*mo2480*	similar to acetyltransferase	2.41	
lmo2482 (lgt)	highly similar to prolipoprotein diacylglyceryl transferase	2.01	
lmo2556 (fbaA)	similar to fructose-1,6-bisphosphate aldolase	4.44	
lmo2559 (pyrG)	highly similar to CTP synthases	2.08	
l*mo2659*	similar to ribulose-phosphate 3-epimerase	5.76	
l*mo2660*	similar to transketolase	6.83	
l*mo2661*	similar to ribulose-5 phosphate 3-epimerase	6.8	
lmo2663	similar to polyol dehydrogenase	9.44	
lmo2664	similar to sorbitol dehydrogenase	9.87	
lmo2665	similar to PTS system galactitol-specific enzyme IIC component	4.9	
l*mo2666*	similar to PTS system galactitol-specific enzyme IIB component	7.33	
lmo2667	similar to PTS system galactitol-specific enzyme IIA component	9.39	
lmo2743	similar to transaldolase	4.23	
lmo2797	similar to PTS mannitorl-specific enzyme IIA	2.94	
l*mo2798*	similar to phosphatase	2.28	
lmo2799	similar to PTS mannitol-specific enzyme IIBC	2.21	
lmo2841	weakly similar to sucrose phosphorylase		2.01
Motility			
lmo0677	similar to flagellar biosynthesis protein FliQ	2.84	
lmo0679	similar to flagellar biosythnesis protein flhB	2.3	
lmo0689	similar to CheA activity-modulating chemotaxis protein CheV	2.01	
lmo0690 (flaA)	flagellin protein	2.16	
Signal transduction			
lmo0287	similar to two-component response regulator	3.45	
lmo1172	similar to two-component response regulator		2.05
lmo1270	similar to signal peptidase I	2.89	

	lmo1378 (lisK)	two-component sensor histidine kinase	2.23	
?	l*mo1558*	similar to hypothetical GTP binding protein	2.05	
	l*mo1699*	some similarities to metyl-accepting chemotaxis proteins	2	
	lmo1800	similar to protein-tyrosine phosphatase		2.11
	l*mo2010*	similar to two-component response regulator	2.12	
	l*mo2421*	similar to two-component sensor histidine kinase	2.08	

Replication, Transcription, Translation

lmo0001 (dnaA)	Chromosomal replication initiation protein DnaA	2.13	
lmo0162	similar to *B. subtilis* DNA polymerase III (delta subunit)	2.19	
lmo0248 (rplK)	ribosomal protein L11	2.81	
lmo0249 (rplA)	ribosomal proteins L1	2.67	
lmo0520	similar to transcription regulator		2.09
lmo0866	similar to ATP-dependent RNA helicase	2.98	
lmo0890 (rsbS)	highly similar to negative regulation of sigma-B activity	2.36	
lmo0891 (rsbT)	highly similar to positive regulation of sigma-B activity	2.23	
lmo0918	similar to transcription antiterminator BglG family		2.1
l*mo1067*	similar to GTP-binding elongation family	3.34	
lmo1278 (clpQ)	highly similar to beta-type subunit of the 20S proteasome	2.17	
lmo1286 (parE)	highly similar to DNA gyrase-like protein (subunit B)	3.49	
lmo1287 (parC)	highly similar to DNA gyrase-like protein (subunit A)	2.64	
lmo1330 (rpsO)	ribosomal protein S15	4.37	
lmo1364 (cspL)	similar to cold shock protein	7.01	
lmo1444	similar to protein secretion PrsA (post-translocation molecular chaperone)		2.41
lmo1479 (lepA)	highly similar to GTP-binding protein LepA	3.26	
lmo1480 (rpsT)	ribosomal protein S20	2.88	
lmo1540 (rpmA)	ribosomal protein L27	3.16	
lmo1542 (rplU)	ribosomal protein L21	3.29	
lmo1722	similar to ATP-dependent RNA helicase	3.86	
lmo1783 (rplT)	ribosomal protein L20	2.15	
lmo1784 (rpmT)	ribosomal protein L35	2.8	

lmo1785 (infC)	translation initiation factor IF-3	2.17	
lmo1787 (rpiS)	ribosomal protein L19	2.39	
lmo1850	similar to transcriptional regulator (MarR family)	2.47	
l*mo1859*	similar to transcriptional regulator (PilB family)	3.89	
l*mo1881*	similar to 5'-3' exonuclease	4.25	
lmo1882	similar to ribosomal protein S14	6.17	
l*mo1938*	similar to ribosomal protein S1 like protein	3.07	
lmo2219	similar to post-translocational molecular chaperone	4.2	
l*mo2366*	similar to transcriptional regulator DeoR family		2.17
l*mo2428*	similar to cell division proteins RodA, FtsW	2.55	
lmo2460	similar to *B. subtilis* CggR hypothetical transcriptional protein	4.43	
lmo2620 (rplE)	ribosomal protein L5	2.15	
lmo2627 (rplV)	ribosomal protein L22	2.14	
lmo2654 (fus)	highly similar to translational elongation factor G	2.23	
l*mo2668*	similar to transcriptional antiterminator (BglG family)	7.44	
lmo2795	similar to *E. coli* RpiR transcription regulator	2.34	
lmo2856 (rpmH)	ribosomal protein L34	2.95	

Other hypothetical proteins

lmo0047	unknown	5.6	
lmo0134	similar to *E. coli* YjdJ protein		2.22
lmo0174	similar to transposases		2.15
lmo0189	highly similar to *B. subtilis* Veg protein	5.2	
lmo0222	conserved hypothetical protein	2.13	
lmo0306	hypothetical protein		2.36
lmo0329	similar to transposase		2.27
lmo0377	unknown	2.4	
lmo0391	unknown	4.13	
lmo0392	highly similar to *B. subtilis* YqfA protein	2.77	
lmo0393	unknown	3.78	

lmo0403	unknown	2.09	
lmo0415	similar to endo-1,4-beta-xylase	5.46	
lmo0452	similar to unknown proteins	2.85	
lmo0453	conserved hypothetical protein	3.05	
lmo0454	conserved hypothetical protein similar to *B. subtilis* YeaC	3.43	
lmo0478	putative secreted protein	2.34	
lmo0553	unknown	2.07	
lmo0563 (hisF)	highly similar to cyclase HisF	2.93	
lmo0589	hypothetical protein		2
lmo0590	similar to a fusion of two types of conserved hypothetical protein		2.08
l*mo0591*	similar to unknown membrane proteins		2.12
lmo0592	unknown	2.45	
l*mo0604*	similar to *B. subtilis* YvlA protein	3.54	
lmo0609	similar to *E. coli* phage shock protein E	4.87	
l*mo0624*	acetyltransferase, GNAT family	2.12	
l*mo0644*	similar to conserved hypothetical proteins	2.94	
l*mo0655*	similar to phosphoprotein phosphatases		2.05
l*mo0665*	unknown	2.08	
l*mo0699*	similar to oxidoreductase		2.97
lmo0688	similar to unknown protein	2.71	
lmo0724	similar to *B. subtilis* YvpB protein	4.1	
lmo0746	hypothetical protein		2.15
lmo0747	hypothetical protein		3.09
lmo0794	similar to *B. subtilis* YwnB protein		2.08
lmo0799	unknown	2.11	
lmo0800	similar to B. subtilis YqkB protein	2.59	
lmo0823	similar to oxidoreductases	16.99	
lmo0827	similar to transposases		2.32
lmo0832	similar to transposase		3.56
lmo0860	similar to sugar ABC transporter, permease protein		2.48

lmo0861	similar to sugar ABC transporter, permease protein		2.18
lmo0905	unknown	3.09	
lmo0906	similar to glutathione reductase	3.86	
lmo0907	similar to phosphoglycerate mutase	3.72	
l*mo0954*	unknown	4.98	2.64
lmo0955	unknown	3.19	2.88
lmo0979	similar to daunorubicin resistance ATP-binding protein		2.02
lmo0987	similar to *Streptococcus agalactiae* CylB protein	2.1	
lmo0990	conserved hypothetical protein		2.06
lmo1026	similar to *B. subtilis* LytR protein	2.62	
lmo1027	similar to conserved hypothetical proteins (in particular *B. subtilis* YkqC)	3.54	
lmo1037	highly similar to B. subtilis YoaT protein		2.37
lmo1040	similar to molybdenum ABC transporters (permease)	2.09	
lmo1137	hypothetical protein	2.66	
lmo1139	hypothetical protein	2.37	
lmo1140	hypothetical protein	2.1	
lmo1146	hypothetical protein	2.16	
lmo1190	hypothetical protein		2.81
lmo1233 (trxA)	thioredoxin	2.95	
lmo1234 (uvrC)	highly similar to exinuclease ABC subunit C	2.22	
lmo1241	hypothetical protein		2
lmo1245	unknown	4.62	
lmo1257	unknown	2.9	
lmo1264	hypothetical protein		2.49
lmo1267 (tig)	trigger factor (prolyl isomerase)	3.21	
lmo1279 (clpY)	highly similar to ATP-dependent Clp protease-like proteins	2.7	
lmo1280 (codY)	highlt similar to *B. subtilis* CodY protein	2.52	
lmo1285	conserved hypothetical protein, similar to *B. subtilis* YneT protein	2.7	
lmo1318	conserved hypothetical protein similar to *B. subtilis* YluC protein	2.04	
lmo1333	similar to *B. subtilis* YqzC protein	2.76	

lmo1334	similar to *B. subtilis* YqzD protein	2.38	
lmo1341	weakly similar to *B. subtilis* operon protein 7 (comGG)		2.39
lmo1342	similar to *B. subtilis* comG protein 6		2.49
lmo1343	similar to comG protein 5 (comGE)		2.42
lmo1344	similar to comG protein 4 (comGD)		2.7
lmo1345	similar to B. subtilis comG operon protein 3		2.07
lmo1351	unknown	2.83	
lmo1352	unknown	2.46	
lmo1353	similar to B. subtilis YqhQ protein 3	2.51	
lmo1362	similar to exodeoxyribonuclease small subunit	3.67	
lmo1384	similar to unknown protein	2.01	
lmo1389	similar to unknown protein	2.19	
lmo1416	unknown	2.05	
lmo1431	similar to ABC transporter (ATP-binding protein)	2.13	
lmo1433	similar to glutathione reductase		2.15
lmo1440	similar to unknown proteins	3.99	
lmo1449	similar to endonuclease IV	2.1	
lmo1486	unknown	2.15	
lmo1487	similar to unknown proteins	3	
lmo1491	similar to unknown proteins	2.47	
l*mo1517*	similar to nitrogen regulatory PII protein	2.02	
lmo1539	similar to glycerol uptake facilitator		2.05
lmo1541	similar to unknown protein	3.94	
lmo1575	similar to unknown protein	2.09	
lmo1595	GAF domain-containing protein	2.45	
lmo1612	similar to unknown proteins	2.52	
lmo1623	similar to unknown proteins	2.07	
lmo1649	unknown	4.15	
lmo1650	similar to hypothetical proteins	2.24	
lmo1655	similar to unknown proteins		3.83

l*mo1670*	similar to conserved hypothetical proteins	3.95	
lmo1674	similar to prolyl aminopeptidases	2.86	
lmo1690	similar to hypothetical proteins	2.14	
lmo1843	similar to conserved hypothetical proteins	2.31	
lmo1845	similar to conserved hypothetical proteins	2.34	
lmo1855	similar to D-alanyl-D-alanine caroxypeptidases	3.71	
lmo1860	similar to peptidyl methionine sulfoxide reductases	3.03	
lmo1874	similar to thymidylate synthase	2.22	
l*mo1914*	similar to unknown proteins	2.14	
lmo1916	similar to peptidase	2.11	
lmo1918	similar to unknown proteins	2	
lmo1937	similar to unknown proteins	5.44	
l*mo1955*	similar to integrase/recombinase	2.25	
lmo1958	similar to ferrichrome ABC transporter (permease)		2.1
lmo1959	similar to ferrichrome binding protein		2.04
lmo1963	similar to unknown proteins	2.05	
lmo1967	similar to toxic resistance proteins	2.82	
l*mo2012*	similar to unknown proteins		2.15
lmo2029	similar to unknown proteins	2.24	
lmo2065	unknown	2.46	
lmo2066	unknown	2.68	
lmo2067	similar to conjugated bile acid hydrolase		2.08
lmo2072	similar to putative DNA binding proteins	6.85	
lmo2131	hypothetical protins		2.12
lmo2152	similar to thioredoxin	4.04	
lmo2154	similar to ribonucleoside-diphosphate reductase, subunit beta	2.39	
lmo2155	similar to ribonucleoside-diphosphate reductase, subunit alpha	2.01	
lmo2157	hypothetical protein		2.15
lmo2180	similar to unknown protein		2.59
l*mo2183*	similar to ferrichrome ABC transporter (premease)		2.28

lmo2194 (oppC)	similar to oligopeptide ABC transporter (permease)		2.3	
lmo2196 (oppA)	similar to pheromone ABC transporter (binding protein)	2.6		
lmo2212 (hemE)	similar to uroporphyrinogen III decarboxylase		2.02	
lmo2217	similar to unknown protein		2.58	
lmo2256	similar to unknown proteins		2.45	
lmo2258	unknown		2.64	
lmo2263	similar to unknown proteins		2.4	
lmo2356	hypothetical protein			2.06
lmo2394	hypothetical CDS			3.3
lmo2412	similar to conserved hypothetical proteins		2.97	
lmo2414	similar to aminotransferase		2.3	
lmo2434	highly similar to glutamate decarboxylases			2.34
l*mo2481*	similar to B. subtilis P-Ser-HPr-phosphatase		2.54	
lmo2487	similar to B. subtilis YvlB protein		3.27	2.1
lmo2502	unknown		2.61	
lmo2503	similar to cardiolipin synthase		2.13	
lmo2507 (ftsE)	highly similar to cell-division ATP-binding protein		3.7	
lmo2506 (ftsX)	highly similar to cell-division protein FtsX		3.62	
lmo2529 (atpD)	highly similar to H+-transporting ATP synthase chain beta		2.06	
lmo2533 (atpF)	highly similar to H+-transporting ATP synthase chain b		2.39	
lmo2532 (atpH)	highly similar to H+-transporting ATP synthase chain delta		2.06	
lmo2567	unknown		2.01	
lmo2682	highly similar to potassium-transporting ATPase A chain			2.39
lmo2683	similar to cellobiose phosphotoransferase enzyme IIB component		2.19	
lmo2685	similar to cellobiose phosphotoransferase enzyme IIA component		2.4	
lmo2688	similar to cell division protein FtsW			2.02
lmo2691	similar to autolysin, N-acetlymuramidase		2.05	
lmo2695	similar to dihydroxacetone kinase			2.21
lmo2713	secreted protein with 1 GW repeat		3.42	
l*mo2742*	unknown		2.88	

lmo2809	hypothetical secreted protein	2.94	
lmo2815	similar to reductases	2.03	
lmo2850	similar to sugar transport proteins		2.33